separating the amplification products, by gel electrophoresis under denaturing conditions, to produce electrophoresis profiles and

comparing the electrophoresis profiles obtained with mixtures of fragments derived from resistant descendants and mixtures derived from sensitive descendants, with fragments derived from parental varieties, for the purpose of identifying bands whose polymorphism is genetically linked to the resistance locus, this identification optionally being followed, for validation purposes, by verification on each individual and calculation of the genetic recombination rate between the marker and the resistance locus.

A1 cont'd

2. (Amended) Method according to claim 1, wherein the DNA fragments are obtained by digestion of the genomic DNA of resistant plants and of sensitive plants, and their parents, using restriction enzymes.

3. (Amended) Method according to claim 2, wherein said restriction enzymes are at least one of EcoRI and MseI.

4. (Amended) Method according to claim 2, wherein the restriction fragments are ligated to adapters.

5. (Amended) Method according to claim 4, wherein the fragments obtained are amplified using primer pairs complementary to the adapters, whose sequences are respectively GAC TGC GTA CCA ATT C(SEQ ID N°1) and GAT GAG TCC TGA GTA A(SEQ ID N°2).

6. (Amended) Method according to claim 4, wherein the fragments obtained are amplified using primer pairs having at their end the respective motifs AAC and CAG, ACC and CAG, and optionally also AGC and CAG.

7. (Amended) Method according to claim 1, further comprising identifying resistance marker bands, M1 and M2, whose size is respectively 510 bp and 140 bp.

8. (Amended) Method according to claim 7, wherein said marker bands determine a segment of less than 10-15 cM carrying the resistance locus.

9. (Amended) Method according to claim 8, wherein said marker bands are located either side of the locus at less than 5-10 cM.

10. (Amended) Method according to claim 7, further comprising isolating said identified marker bands.

11. (Amended) Method according to claim 10, further comprising purifying the isolated marker bands in order to obtain DNA fragments.

12. (Amended) Method according to claim 11, further comprising cloning the marker bands into a vector and insertion of the vector in a host cell.

13. (Amended) Method according to claim 11, further comprising recovering and sequencing the purified, cloned DNA fragments.

14. (Amended) Method for obtaining markers having high specificity for the locus of a major RYMV resistance gene, comprising cloning and amplifying cloned fragments of said locus with PCR primer pairs which are complementary to the sequence of the cloned fragment, and subjecting amplification products to migration on an

electrophoresis gel with or without previous digestion of said amplification products by a restriction enzyme, to identify a polymorphism.

15. (Amended) A Polymorphous AFLP band identified by the method according to claim 1 using rice plant DNA.

16. (Amended) An AFLP band according to claim 15, wherein said rice plant is a RYMV-sensitive variety, or a plant which is the progeny of an RYMV-sensitive plant and a resistant variety.

17. (Amended) A DNA sequence corresponding to a polymorphous band according to claim 15 or 16, which can be used to define a segment of chromosome 4 of 10-15 cM carrying the RYMV resistance locus.

18. (Amended) A DNA sequence according to claim 17, which is an EcoRI-MseI fragment.

19. (Amended) A DNA sequence according to claim 18, which is between 510 bp and 140 bp, determined by gel electrophoresis under denaturing conditions.

20. (Amended) A DNA sequence according to claim 17 which is a sequence flanking the resistance locus within a distance of 10 cM.

21. (Amended) A DNA sequence of SEQ ID N°3 or SEQ ID N°:9.

23. (Amended) A cloning vector comprising at least one of sequence SEQ ID N°3 according to claim 21 and SEQ ID N°9.

24. (Amended) A host cell transformed by a vector according to claim 23.

25. (Amended) Use of polymorphous bands according to claim 15 for the identification of resistant phenotypes and transfer of the resistance gene.